



#4

SEQUENCE LISTING

<110> Padigaru, Muralidhara
Gerlach, Valerie L.
Smithson, Glennda
Stone, David
Bin-Yang, Ruey
Conley, Pamela B.
Hart, Matthew
Tomlinson, James E.
Topper, James N.
Kekuda, Ramesh
Casman, Stacie J.
MacDougall, John R.
Edinger, Shlomit R.

<120> Novel GPCR-Like Proteins and Nucleic Acids Encoding
Same

<130> 21402-224 AG

<140> 10/024444

<141> 2001-12-18

<150> 60/256635

<151> 2000-12-18

<160> 12

<170> PatentIn Ver. 2.1

<210> 1

<211> 977

<212> DNA

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: Unknown

<400> 1

gcaactaaaa aaacacatca tggagctccg gaactccacc ttgggaagcg gcttcatctt 60
ggtgtggatt ctgaatgaca gtgggtctcc tgaactgctc tatgctacat ttacaatctt 120
atacatgttg gcactgacca gcaatggctc gctgctccctg gccatcacca tagaagccccg 180
gctccacatg cccatgttacc tcctgcttgg gcagctctct ctcatggacc tcctgttcac 240
atctgttgc actcccaagg ctttggcgga ctttctgcgc agagaaaaca ctatctccctt 300
tggaggctgt gcacttcaga ttttcttggc actgacaatg gtagcgctg aggacccctt 360
actggccttc atggcttatg acaggtatgt ggccattttgt catcctctga aatacatgac 420
cctcatgagc ccaagagtct gctggatcat ggtggccaca tcctggatcc tggcatccct 480
gattgctata ggacatacca tgtacactat gcacccctt ttctgtgtt cctggaaat 540
caggcatctg ctctgtgaga tcccacccctt gctgaagttt gcctgtgtt atacccctt 600
gtatgagctt ataataatacg tgacaggtgt gacttccctt ttgtccccca ttctgtccat 660
tgtggccctt tacacactag tccttattcac tgtgcttcgt atgccatcaa atgaggggag 720
gaagaaaagcc cttgtcacct gctttccca cctgattgtt gtcgggatgt tctatggagc 780
tgccacatcc atgtatgttcc ttcccacccgc cccaaacaag acaacatcat 840
ctctgttttc tacacaatttgc tcaactccagc cctgaatcca ctcatctaca gcctgaggaa 900
taaggagggtc atgcgggcct tgaggagggtt cctggggaaaa tacatactgc tggcacattc 960
cacgctctag ggaagga 977

<210> 2
<211> 316
<212> PRT
<213> Unknown Organism

<220>
<223> Description of Unknown Organism: Unknown

<400> 2
Met Glu Leu Arg Asn Ser Thr Leu Gly Ser Gly Phe Ile Leu Val Gly
1 5 10 15
Ile Leu Asn Asp Ser Gly Ser Pro Glu Leu Leu Tyr Ala Thr Phe Thr
20 25 30
Ile Leu Tyr Met Leu Ala Leu Thr Ser Asn Gly Leu Leu Leu Ala
35 40 45
Ile Thr Ile Glu Ala Arg Leu His Met Pro Met Tyr Leu Leu Leu Gly
50 55 60
Gln Leu Ser Leu Met Asp Leu Leu Phe Thr Ser Val Val Thr Pro Lys
65 70 75 80
Ala Leu Ala Asp Phe Leu Arg Arg Glu Asn Thr Ile Ser Phe Gly Gly
85 90 95
Cys Ala Leu Gln Met Phe Leu Ala Leu Thr Met Gly Ser Ala Glu Asp
100 105 110
Leu Leu Leu Ala Phe Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His
115 120 125
Pro Leu Lys Tyr Met Thr Leu Met Ser Pro Arg Val Cys Trp Ile Met
130 135 140
Val Ala Thr Ser Trp Ile Leu Ala Ser Leu Ile Ala Ile Gly His Thr
145 150 155 160
Met Tyr Thr Met His Leu Pro Phe Cys Val Ser Trp Glu Ile Arg His
165 170 175
Leu Leu Cys Glu Ile Pro Pro Leu Leu Lys Leu Ala Cys Ala Asp Thr
180 185 190
Ser Arg Tyr Glu Leu Ile Ile Tyr Val Thr Gly Val Thr Phe Leu Leu
195 200 205
Leu Pro Ile Ser Ala Ile Val Ala Ser Tyr Thr Leu Val Leu Phe Thr
210 215 220
Val Leu Arg Met Pro Ser Asn Glu Gly Arg Lys Lys Ala Leu Val Thr
225 230 235 240
Cys Ser Ser His Leu Ile Val Val Gly Met Phe Tyr Gly Ala Ala Thr

245	250	255
Phe Met Tyr Val Leu Pro Ser Ser Phe His Ser Pro Lys Gln Asp Asn		
260	265	270
Ile Ile Ser Val Phe Tyr Thr Ile Val Thr Pro Ala Leu Asn Pro Leu		
275	280	285
Ile Tyr Ser Leu Arg Asn Lys Glu Val Met Arg Ala Leu Arg Arg Val		
290	295	300
Leu Gly Lys Tyr Ile Leu Leu Ala His Ser Thr Leu		
305	310	315
<210> 3		
<211> 316		
<212> PRT		
<213> human		
<400> 3		
Met Glu Leu Trp Asn Phe Thr Leu Gly Ser Gly Phe Ile Leu Val Gly		
1	5	10
		15
Ile Leu Asn Asp Ser Gly Ser Pro Glu Leu Leu Cys Ala Thr Ile Thr		
20	25	30
Ile Leu Tyr Leu Leu Ala Leu Ile Ser Asn Gly Leu Leu Leu Ala		
35	40	45
Ile Thr Met Glu Ala Arg Leu His Met Pro Met Tyr Leu Leu Leu Gly		
50	55	60
Gln Leu Ser Leu Met Asp Leu Leu Phe Thr Ser Val Val Thr Pro Lys		
65	70	75
		80
Ala Leu Ala Asp Phe Leu Arg Arg Glu Asn Thr Ile Ser Phe Gly Gly		
85	90	95
Cys Ala Leu Gln Met Phe Leu Ala Leu Thr Met Gly Gly Ala Glu Asp		
100	105	110
Leu Leu Leu Ala Phe Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His		
115	120	125
Pro Leu Thr Tyr Met Thr Leu Met Ser Ser Arg Ala Cys Trp Leu Met		
130	135	140
Val Ala Thr Ser Trp Ile Leu Ala Ser Leu Ser Ala Leu Ile Tyr Thr		
145	150	155
		160
Val Tyr Thr Met His Tyr Pro Phe Cys Arg Ala Gln Glu Ile Arg His		
165	170	175
Leu Leu Cys Glu Ile Pro His Leu Leu Lys Val Ala Cys Ala Asp Thr		
180	185	190

Ser Arg Tyr Glu Leu Met Val Tyr Val Met Gly Val Thr Phe Leu Ile
 195 200 205
 Pro Ser Leu Ala Ala Ile Leu Ala Ser Tyr Thr Gln Ile Leu Leu Thr
 210 215 220
 Val Leu His Met Pro Ser Asn Glu Gly Arg Lys Lys Ala Leu Val Thr
 225 230 235 240
 Cys Ser Ser His Leu Thr Val Val Gly Met Phe Tyr Gly Ala Ala Thr
 245 250 255
 Phe Met Tyr Val Leu Pro Ser Ser Phe His Ser Thr Arg Gln Asp Asn
 260 265 270
 Ile Ile Ser Val Phe Tyr Thr Ile Val Thr Pro Ala Leu Asn Pro Leu
 275 280 285
 Ile Tyr Ser Leu Arg Asn Lys Glu Val Met Arg Ala Leu Arg Arg Val
 290 295 300
 Leu Gly Lys Tyr Met Leu Pro Ala His Ser Thr Leu
 305 310 315

<210> 4
 <211> 316
 <212> PRT
 <213> mouse

<400> 4
 Met Glu Leu Trp Asn Ser Thr Leu Glu Ser Gly Phe Ile Leu Val Gly
 1 5 10 15
 Ile Leu Asn Gly Ser Ser Pro Glu Leu Leu Cys Ala Ile Val Thr
 20 25 30
 Ala Leu Tyr Met Leu Ala Leu Ile Ser Asn Gly Leu Leu Leu Val
 35 40 45
 Ile Thr Val Asp Ala Arg Leu His Val Pro Met Tyr Leu Leu Leu Arg
 50 55 60
 Gln Leu Ser Leu Ile Asp Leu Leu Phe Thr Ser Val Val Thr Pro Lys
 65 70 75 80
 Ala Val Met Asp Phe Leu Leu Arg Asp Asn Thr Ile Ser Phe Gly Gly
 85 90 95
 Cys Ala Leu Gln Met Ala Leu Ala Leu Met Leu Gly Ser Ala Glu Asp
 100 105 110
 Leu Leu Leu Ala Phe Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His
 115 120 125
 Pro Leu Asn Tyr Met Val Phe Met Ser Pro Thr Val Cys Trp Leu Ile
 130 135 140

Val Ser Thr Ser Trp Ile Leu Ala Ser Leu Thr Ala Val Gly His Thr
 145 150 155 160
 Val Tyr Thr Met His Phe Pro Phe Cys Met Ser Gln Glu Ile Arg His
 165 170 175
 Leu Leu Cys Glu Ile Leu Pro Leu Leu Lys Leu Ser Cys Val Asp Thr
 180 185 190
 Ser Gln Tyr Glu Leu Met Val Tyr Val Thr Gly Val Thr Phe Leu Leu
 195 200 205
 Leu Pro Leu Ser Ala Ile Val Thr Ser Tyr Thr Leu Ile Leu Ser Thr
 210 215 220
 Val Leu His Met Pro Ser Asn Glu Gly Lys Lys Lys Ala Leu Val Thr
 225 230 235 240
 Cys Leu Ser His Leu Met Val Val Gly Met Phe Tyr Gly Ala Ala Thr
 245 250 255
 Phe Met Tyr Val Leu Pro Ser Ser Leu His Ser Ala Lys Gln Asp Asn
 260 265 270
 Ile Ile Ser Val Phe Tyr Thr Ile Val Thr Pro Ala Leu Asn Pro Leu
 275 280 285
 Ile Tyr Ser Leu Arg Asn Lys Glu Val Ile Gly Ala Leu Arg Arg Val
 290 295 300
 Leu Gly Arg Tyr Ile Leu Pro Ala His Leu Thr Leu
 305 310 315

 <210> 5
 <211> 316
 <212> PRT
 <213> mouse

 <400> 5
 Met Glu Pro Trp Asn Ser Thr Leu Glu Ser Gly Phe Ile Leu Val Gly
 1 5 10 15
 Ile Leu Asp Gly Ser Gly Ser Pro Glu Leu Leu Cys Ala Thr Val Thr
 20 25 30
 Thr Leu Tyr Met Leu Ala Leu Ile Ser Asn Gly Leu Leu Leu Val
 35 40 45
 Ile Thr Val Asp Ala Arg Leu His Val Pro Met Tyr Leu Leu Leu Arg
 50 55 60
 Gln Leu Ser Leu Ile Asp Leu Leu Phe Thr Ser Val Val Thr Pro Asn
 65 70 75 80
 Thr Val Val Asp Phe Leu Leu Arg Asp Asn Thr Ile Ser Phe Glu Gly

85

90

95

Cys Ala Leu Gln Leu Leu Phe Ser Ala Met Thr Leu Gly Gly Ala Glu Asp
 100 105 110

Leu Leu Leu Ala Phe Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His
 115 120 125

Pro Leu Asn Tyr Met Ile Phe Met Ser Pro Lys Ala Cys Arg Leu Met
 130 135 140

Val Ala Ile Ser Trp Ile Leu Ala Ser Leu Ser Ala Leu Gly His Thr
 145 150 155 160

Val Tyr Thr Met His Phe Pro Phe Cys Met Ser Gln Glu Ile Arg His
 165 170 175

Leu Leu Cys Glu Val Pro Pro Leu Leu Lys Leu Ala Cys Ala Asp Thr
 180 185 190

Ser Gln Tyr Glu Leu Met Val Tyr Val Thr Gly Val Ile Phe Leu Leu
 195 200 205

Leu Pro Leu Ser Ala Ile Ile Thr Ser Tyr Ser Leu Ile Leu Phe Thr
 210 215 220

Val Leu His Met Pro Ser Asn Glu Gly Arg Lys Lys Ala Leu Val Thr
 225 230 235 240

Cys Ser Ser His Leu Thr Val Val Gly Met Phe Tyr Gly Gly Ala Thr
 245 250 255

Phe Met Tyr Val Leu Pro Ser Ser Phe His Ser Pro Lys Gln Asp Asn
 260 265 270

Ile Ile Ser Val Phe Tyr Thr Ile Val Thr Pro Ala Leu Asn Pro Leu
 275 280 285

Ile Tyr Ser Leu Arg Asn Lys Glu Val Ile Gly Ala Val Arg Arg Val
 290 295 300

Leu Gly Arg His Ile Leu Pro Ala His Ala Thr Val
 305 310 315

<210> 6
 <211> 316
 <212> PRT
 <213> mouse

<400> 6
 Met Glu Pro Trp Asn Ser Thr Leu Glu Ser Gly Phe Ile Leu Val Gly
 1 5 10 15

Ile Leu Asp Gly Ser Gly Ser Pro Glu Leu Leu Cys Ala Thr Val Thr
 20 25 30

Thr Leu Tyr Met Leu Ala Leu Ile Ser Asn Gly Leu Leu Leu Leu Val
 35 40 45

 Ile Thr Val Asp Ala Arg Leu His Val Pro Met Tyr Leu Leu Leu Arg
 50 55 60

 Gln Leu Ser Leu Ile Asp Leu Leu Phe Thr Ser Val Val Thr Pro Asn
 65 70 75 80

 Thr Val Val Asp Phe Leu Leu Arg Asp Asn Thr Ile Ser Phe Glu Gly
 85 90 95

 Cys Ala Leu Gln Leu Phe Ser Ala Met Thr Leu Gly Gly Ala Glu Glu
 100 105 110

 Leu Leu Leu Ala Phe Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His
 115 120 125

 Pro Leu Asn Tyr Met Ile Phe Met Ser Pro Lys Ala Cys Arg Leu Met
 130 135 140

 Val Ala Ile Ser Trp Ile Leu Ala Ser Leu Ser Ala Leu Gly His Thr
 145 150 155 160

 Val Tyr Thr Met His Phe Pro Phe Cys Met Ser Gln Glu Ile Arg His
 165 170 175

 Leu Leu Cys Glu Val Pro Pro Leu Leu Lys Leu Ala Cys Ala Asp Thr
 180 185 190

 Ser Gln Tyr Glu Leu Met Val Tyr Val Thr Gly Val Ile Phe Leu Leu
 195 200 205

 Leu Pro Leu Ser Ala Ile Ile Thr Ser Tyr Ser Leu Ile Leu Phe Thr
 210 215 220

 Val Leu His Met Pro Ser Asn Glu Gly Arg Lys Lys Ala Leu Val Thr
 225 230 235 240

 Cys Ser Ser His Leu Thr Val Val Gly Met Phe Tyr Gly Gly Ala Thr
 245 250 255

 Phe Met Tyr Val Leu Pro Ser Ser Phe His Ser Pro Lys Gln Asp Asn
 260 265 270

 Ile Ile Ser Val Phe Tyr Thr Ile Val Thr Pro Ala Leu Asn Pro Leu
 275 280 285

 Ile Tyr Ser Leu Arg Asn Lys Glu Val Ile Gly Ala Val Arg Arg Val
 290 295 300

 Leu Gly Arg His Ile Leu Pro Ala His Ala Thr Val
 305 310 315

<210> 7
 <211> 316

<212> PRT

<213> mouse

<400> 7

Met Glu Pro Trp Asn Ser Thr Leu Gly Thr Asp Phe Asn Leu Val Gly
1 5 10 15

Ile Leu Asp Asp Ser Gly Ser Pro Glu Leu Leu Cys Ala Thr Phe Thr
20 25 30

Ala Leu Tyr Met Leu Ala Leu Ile Ser Asn Gly Leu Leu Ile Leu Val
35 40 45

Ile Thr Met Asp Ala Arg Leu His Val Pro Met Tyr Phe Leu Leu Gly
50 55 60

Gln Leu Ser Leu Met Asp Leu Leu Phe Thr Ser Val Val Thr Pro Lys
65 70 75 80

Ala Val Ile Asp Phe Leu Leu Arg Asp Asn Thr Ile Ser Phe Glu Gly
85 90 95

Cys Ser Leu Gln Met Phe Leu Ala Leu Thr Leu Gly Gly Ala Glu Asp
100 105 110

Leu Leu Leu Ala Phe Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His
115 120 125

Pro Leu Asn Tyr Met Ile Phe Met Arg Pro Ser Ile Cys Trp Leu Met
130 135 140

Val Ala Thr Ser Trp Val Leu Ala Ser Leu Met Ala Leu Gly Tyr Thr
145 150 155 160

Thr Tyr Thr Met Gln Tyr Ser Tyr Cys Lys Ser Arg Lys Ile Arg His
165 170 175

Leu Leu Cys Glu Ile Pro Pro Leu Leu Lys Leu Ala Cys Ala Asp Thr
180 185 190

Ser Lys Tyr Glu Leu Met Val Tyr Val Met Gly Val Thr Phe Leu Ile
195 200 205

Pro Pro Leu Ala Ala Ile Leu Ala Ser Tyr Ser Leu Ile Leu Phe Thr
210 215 220

Val Leu His Met Pro Ser Asn Glu Gly Arg Lys Lys Ala Leu Val Thr
225 230 235 240

Cys Ser Ser His Leu Thr Val Val Gly Met Phe Tyr Gly Ala Ala Thr
245 250 255

Phe Met Tyr Val Leu Pro Asn Ser Phe His Ser Pro Arg Gln Asp Asn
260 265 270

Ile Ile Ser Val Phe Tyr Thr Ile Val Thr Pro Ala Leu Asn Pro Leu
275 280 285

Ile Tyr Ser Leu Arg Asn Lys Glu Val Thr Gly Ala Leu Ile Arg Val
290 295 300

Leu Gly Arg Tyr Ile Val Pro Ala His Pro Thr Leu
305 310 315

<210> 8
<211> 17
<212> PRT
<213> Unknown Organism

<220>
<223> Description of Unknown Organism: Protein motif

<220>
<221> VARIANT
<222> (1)
<223> X1 wherein X aa is G, or S, or T, or A, or L, or
I, or V, or M, or F, or Y, or W, or C

<220>
<221> VARIANT
<222> (2)
<223> X2 wherein X aa is G, or S, or T, or A, or N, or
C, or C, or P, or D, or E

<220>
<221> VARIANT
<222> (3)
<223> X3 wherein X aa is E, or D, or P, or K, or R, or H

<220>
<221> VARIANT
<222> (4)
<223> X4 wherein X aa is any amino acid

<220>
<221> VARIANT
<222> (5)
<223> X5 wherein X aa is any amino acid

<220>
<221> VARIANT
<222> (6)
<223> X6 wherein X aa is L, or I, or V, or M, or N, or
Q, or G, or A

<220>
<221> VARIANT
<222> (7)
<223> X7 wherein X aa is any amino acid

<220>
<221> VARIANT
<222> (8)

<223> X8 wherein X aa is any amino acid

<220>

<221> VARIANT

<222> (9)

<223> X9 wherein X aa is L, or I, or V, or M, or F, or T

<220>

<221> VARIANT

<222> (10)

<223> X10 wherein X aa is G, or S, or T, or A, or N, or C

<220>

<221> VARIANT

<222> (11)

<223> X11 wherein X aa is L, or I, or V, or M, or F, or Y, or W, or S, or T, or A, or C

<220>

<221> VARIANT

<222> (12)

<223> X12 wherein X aa is D, or E, or N, or H

<220>

<221> VARIANT

<222> (13)

<223> X13 wherein X aa is F, or Y, or W, or W, or C, or S, or H

<220>

<221> VARIANT

<222> (14)

<223> X14 wherein X aa is any amino acid

<220>

<221> VARIANT

<222> (15)

<223> X15 wherein X aa is any amino acid

<220>

<221> VARIANT

<222> (16)

<223> X16 wherein X aa is l, or I, or V, or M

<400> 8
Xaa Arg Xaa Xaa Xaa
1 5 10 15

Xaa

<210> 9
<211> 254
<212> PRT
<213> Unknown Organism

<400> 9

Gly Asn Leu Leu Val Ile Leu Val Ile Leu Arg Thr Lys Lys Leu Arg
1 5 10 15

Thr Pro Thr Asn Ile Phe Leu Leu Asn Leu Ala Val Ala Asp Leu Leu
20 25 30

Phe Leu Leu Thr Leu Pro Pro Trp Ala Leu Tyr Tyr Leu Val Gly Gly
35 40 45

Asp Trp Val Phe Gly Asp Ala Leu Cys Lys Leu Val Gly Ala Leu Phe
50 55 60

Val Val Asn Gly Tyr Ala Ser Ile Leu Leu Leu Thr Ala Ile Ser Ile
65 70 75 80

Asp Arg Tyr Leu Ala Ile Val His Pro Leu Arg Tyr Arg Arg Ile Arg
85 90 95

Thr Pro Arg Arg Ala Lys Val Leu Ile Leu Leu Val Trp Val Leu Ala
100 105 110

Leu Leu Leu Ser Leu Pro Pro Leu Leu Phe Ser Trp Leu Arg Thr Val
115 120 125

Glu Glu Gly Asn Thr Thr Val Cys Leu Ile Asp Phe Pro Glu Glu Ser
130 135 140

Val Lys Arg Ser Tyr Val Leu Leu Ser Thr Leu Val Gly Phe Val Leu
145 150 155 160

Pro Leu Leu Val Ile Leu Val Cys Tyr Thr Arg Ile Leu Arg Thr Leu
165 170 175

Arg Lys Arg Ala Arg Ser Gln Arg Ser Leu Lys Arg Arg Ser Ser Ser
180 185 190

Glu Arg Lys Ala Ala Lys Met Leu Leu Val Val Val Val Phe Val
195 200 205

Leu Cys Trp Leu Pro Tyr His Ile Val Leu Leu Leu Asp Ser Leu Cys
210 215 220

Leu Leu Ser Ile Trp Arg Val Leu Pro Thr Ala Leu Leu Ile Thr Leu
225 230 235 240

Trp Leu Ala Tyr Val Asn Ser Cys Leu Asn Pro Ile Ile Tyr
245 250

<210> 10

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR Primer

<400> 10
tgccacattc atgtatgtct tg

22

<210> 11
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR Primer

<400> 11
cacagccccca aacaagacaa catcat

26

<210> 12
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR Primer

<400> 12
ggctggagtg acaatttgt ag

22